Replacement Sheet

FIGURE 7

Predicted twin-arginine (RR-)signal peptides of B. subtilis[1]

Protein	N	h	RR-Motif	SEQ ID NO:	H	h	C
AlbB	1	0.1	**RRILL**	30	27	2.0	AIA
AmyX™	9	-0.8	**RRSFE**	31	15	1.1	-
AppB™	8	0.5	**RRTLM**	32	19	2.3	-
LipA	7	-1.1	**RRIIA**	33	19	1.2	AKA
OppB™	8	-0.6	**RRLVY**	34	24	2.0	-
PbpX	2	-2.2	**RRRKL**	35	14	2.9	WNA
PhoD	3	-1.3	**RRKFI**	36	17	0.9	VGA
QcrA™	1	-1.1	**RRQFL**	37	19	1.3	-
TlpA™	1	-0.8	**RRLII**	38	21	2.4	-
WapA[W]	1	-3.0	**RRNFK**	39	18	2.3	VLA
WprA	8	-1.7	**RRKFS**	40	20	1.9	AAA
YceA™	1	-0.4	**RRAFL**	41	21	2.2	-
YesM™	1	-1.5	**RRMKI**	42	20	2.4	QYA
YesW	1	-1.3	**RRSCL**	43	19	2.0	VKA
YfkN™	1	-1.2	**RRTHV**	44	17	1.7	IHA
YkpC	8	-1.0	**RRVAI**	45	17	2.3	SLA
YkuE	1	-1.3	**RRQFL**	46	17	1.0	GYA
YmaC	7	0.0	**RRFLL**	47	15	2.4	YSL
YubF™	9	-2.7	**RRNTV**	48	23	2.0	-
YuiC	8	0.2	**RRLLM**	49	20	1.9	IEA
YvhJ™	2	-1.7	**RRKIL**	50	18	2.5	-
YwbN	1	-1.8	**RRDIL**	51	23	1.4	QTA

[1]The listed signal peptides contain, in addition to the twin-arginines, at least one other residue of the consensus sequence (R-R-X-Φ-Φ; printed in bold). The number of residues in the N- and H-domains of each signal peptide, and the average hydrophobicity (h) of each of these domains, as determined by the algorithms of Kyte and Doolittle (Kyte, J., and R. F. Doolittle [1982] A simple method for displaying the hydropathic character of a protein. J. Mol. Biol. 157:105-32), are indicated. Furthermore, the RR-motifs in the N-domain, and SPaseI recognition sites in the C-domain (*ie*. positions -3 to -1 relative to the predicted SPase cleavage site) are shown. Proteins lacking a (putative) SPaseI cleavage site, some of which contain additional transmembrane domains, are indicated with "TM". One protein containing cell wall binding repeats is indicated with "W".